



SEQUENCE LISTING

<110> JENSEN, Ma in Roland et al.

<120> NOVEL METHOD FOR DOWN-REGULATION OF AMYLOID

<130> 3631-0107P

<140> 09/785,215

<141> 2001-02-20

<160> 19

<170> PatentIn version 3.1

<210> 1

<211> 2313

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(2313)

<223>

<220>

<221> misc_feature

<222> (2098)..(2169)

<223> nucleotides encoding transmembrane region

<220>

<221> misc_feature

<222> (2014)..(2313)

<223> Nucleotides encoding C-100

<220>

<221> misc_feature

<222> (2016)..(2144)

<223> Abeta 42/43

<220>

<221> misc_feature

<222> (2014)..(2142)

<223> Abeta 42/43

<400> 1

atg ctg ccc ggt ttg gca ctg ctc ctg ctg gcc gcc tgg acg gct cgg
Met Leu Pro Gly Leu Ala Leu Leu Leu Ala Ala Trp Thr Ala Arg
1 5 10 15

48

gcg ctg gag gta ccc act gat ggt aat gct ggc ctg ctg gct gaa ccc Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro 20 25 30	96
cag att gcc atg ttc tgt ggc aga ctg aac atg cac atg aat gtc cag Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln 35 40 45	144
aat ggg aag tgg gat tca gat cca tca ggg acc aaa acc tgc att gat Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp 50 55 60	192
acc aag gaa ggc atc ctg cag tat tgc caa gaa gtc tac cct gaa ctg Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu 65 70 75 80	240
cag atc acc aat gtg gta gaa gcc aac caa cca gtg acc atc cag aac Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn 85 90 95	288
tgg tgc aag cgg ggc cgc aag cag tgc aag acc cat ccc cac ttt gtg Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val 100 105 110	336
att ccc tac cgc tgc tta gtt ggt gag ttt gta agt gat gcc ctt ctc Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu 115 120 125	384
gtt cct gac aag tgc aaa ttc tta cac cag gag agg atg gat gtt tgc Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys 130 135 140	432
gaa act cat ctt cac tgg cac acc gtc gcc aaa gag aca tgc agt gag Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu 145 150 155 160	480
aag agt acc aac ttg cat gac tac ggc atg ttg ctg ccc tgc gga att Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile 165 170 175	528
gac aag ttc cga ggg gta gag ttt gtg tgt tgc cca ctg gct gaa gaa Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu 180 185 190	576
agt gac aat gtg gat tct gct gat gcg gag gag gat gac tcg gat gtc Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val 195 200 205	624
tgg tgg ggc gga gca gac aca gac tat gca gat ggg agt gaa gac aaa Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys 210 215 220	672
gta gta gaa gta gca gag gag gaa gaa gtg gct gag gtg gaa gaa gaa Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu 225 230 235 240	720

gaa Glu	gcc Ala	gat Asp	gat Asp	gac Asp 245	gag Glu	gac Asp	gat Asp	gag Glu	gat Asp 250	ggt Gly	gat Asp	gag Glu	gta Val	gag Glu 255	gaa Glu	768
gag Glu	gct Ala	gag Glu	gaa Glu 260	ccc Pro	tac Tyr	gaa Glu	gaa Glu	gcc Ala 265	aca Thr	gag Glu	aga Arg	acc Thr 270	acc Thr	agc Ser	att Ile	816
gcc Ala	acc Thr	acc Thr 275	acc Thr	acc Thr	acc Thr	acc Thr	aca Thr 280	gag Glu	tct Ser	gtg Val	gaa Glu	gag Glu 285	gtg Val	gtt Val	cga Arg	864
gag Glu	gtg Val 290	tgc Cys	tct Ser	gaa Glu	caa Gln	gcc Ala 295	gag Glu	acg Thr	ggg Gly	ccg Pro	tgc Cys 300	cga Arg	gca Ala	atg Met	atc Ile	912
tcc Ser 305	cgc Arg	tgg Trp	tac Tyr	ttt Phe	gat Asp 310	gtg Val	act Thr	gaa Glu	ggg Gly	aag Lys 315	tgt Cys	gcc Ala	cca Pro	ttc Phe	ttt Phe 320	960
tac Tyr	ggc Gly	gga Gly	tgt Cys	ggc Gly 325	ggc Gly	aac Asn	cgg Arg	aac Asn	aac Asn 330	ttt Phe	gac Asp	aca Thr	gaa Glu	gag Glu 335	tac Tyr	1008
tgc Cys	atg Met	gcc Ala	gtg Val 340	tgt Cys	ggc Gly	agc Ser	gcc Ala	atg Met 345	tcc Ser	caa Gln	agt Ser	tta Leu	ctc Leu 350	aag Lys	act Thr	1056
acc Thr	cag Gln	gaa Glu 355	cct Pro	ctt Leu	gcc Ala	cga Arg	gat Asp 360	cct Pro	gtt Val	aaa Lys	ctt Leu	cct Pro 365	aca Thr	aca Thr	gca Ala	1104
gcc Ala	agt Ser 370	acc Thr	cct Pro	gat Asp	gcc Ala	gtt Val 375	gac Asp	aag Lys	tat Tyr	ctc Leu	gag Glu 380	aca Thr	cct Pro	ggg Gly	gat Asp	1152
gag Glu 385	aat Asn	gaa Glu	cat His	gcc Ala 390	cat His	ttc Phe	cag Gln	aaa Lys	gcc Ala 395	aaa Lys	gag Glu	agg Arg	ctt Leu	gag Glu	gcc Ala 400	1200
aag Lys	cac His	cga Arg	gag Glu	aga Arg 405	atg Met	tcc Ser	cag Gln	gtc Val	atg Met 410	aga Arg	gaa Glu	tgg Trp	gaa Glu	gag Glu 415	gca Ala	1248
gaa Glu	cgt Arg	caa Gln	gca Ala 420	aag Lys	aac Asn	ttg Leu	cct Pro	aaa Lys 425	gct Ala	gat Asp	aag Lys	aag Lys	gca Ala 430	gtt Val	atc Ile	1296
cag Gln	cat His	ttc Phe 435	cag Gln	gag Glu	aaa Lys	gtg Val	gaa Glu 440	tct Ser	ttg Leu	gaa Glu	cag Gln	gaa Glu 445	gca Ala	gcc Ala	aac Asn	1344
gag Glu	aga Arg 450	cag Gln	cag Gln	ctg Leu	gtg Val	gag Glu 455	aca Thr	cac His	atg Met	gcc Ala	aga Arg	gtg Val 460	gaa Glu	gcc Ala	atg Met	1392

ctc Leu 465	aat Asn	gac Asp	cgc Arg	cgc Arg	cgc Arg	ctg Leu	gcc Ala	ctg Leu	gag Glu	aac Asn	tac Tyr	atc Ile	acc Thr	gct Ala	ctg Leu	1440
					470					475					480	
cag Gln	gct Ala	gtt Val	cct Pro	cct Pro	cgg Arg	cct Pro	cgt Arg	cac His	gtg Val	ttc Phe	aat Asn	atg Met	cta Leu	aag Lys	aag Lys	1488
				485					490					495		
tat Tyr	gtc Val	cgc Arg	gca Ala	gaa Glu	cag Gln	aag Lys	gac Asp	aga Arg	cag Gln	cac His	acc Thr	cta Leu	aag Lys	cat His	ttc Phe	1536
			500					505					510			
gag Glu	cat His	gtg Val	cgc Arg	atg Met	gtg Val	gat Asp	ccc Pro	aag Lys	aaa Lys	gcc Ala	gct Ala	cag Gln	atc Ile	cgg Arg	tcc Ser	1584
		515					520					525				
cag Gln	gtt Val	atg Met	aca Thr	cac His	ctc Leu	cgt Arg	gtg Val	att Ile	tat Tyr	gag Glu	cgc Arg	atg Met	aat Asn	cag Gln	tct Ser	1632
	530					535					540					
ctc Leu 545	tcc Ser	ctg Leu	ctc Leu	tac Tyr	aac Asn	gtg Val	cct Pro	gca Ala	gtg Val	gcc Ala	gag Glu	gag Glu	att Ile	cag Gln	gat Asp	1680
					550					555					560	
gaa Glu	gtt Val	gat Asp	gag Glu	ctg Leu	ctt Leu	cag Gln	aaa Lys	gag Glu	caa Gln	aac Asn	tat Tyr	tca Ser	gat Asp	gac Asp	gtc Val	1728
				565					570					575		
ttg Leu	gcc Ala	aac Asn	atg Met	att Ile	agt Ser	gaa Glu	cca Pro	agg Arg	atc Ile	agt Ser	tac Tyr	gga Gly	aac Asn	gat Asp	gct Ala	1776
			580					585					590			
ctc Leu	atg Met	cca Pro	tct Ser	ttg Leu	acc Thr	gaa Glu	acg Thr	aaa Lys	acc Thr	acc Thr	gtg Val	gag Glu	ctc Leu	ctt Leu	ccc Pro	1824
		595					600					605				
gtg Val	aat Asn	gga Gly	gag Glu	ttc Phe	agc Ser	ctg Leu	gac Asp	gat Asp	ctc Leu	cag Gln	ccg Pro	tgg Trp	cat His	tct Ser	ttt Phe	1872
	610					615					620					
ggg Gly 625	gct Ala	gac Asp	tct Ser	gtg Val	cca Pro	gcc Ala	aac Asn	aca Thr	gaa Glu	aac Asn	gaa Glu	gtt Val	gag Glu	cct Pro	gtt Val	1920
					630					635					640	
gat Asp	gcc Ala	cgc Arg	cct Pro	gct Ala	gcc Ala	gac Asp	cga Arg	gga Gly	ctg Leu	acc Thr	act Thr	cga Arg	cca Pro	ggg Gly	tct Ser	1968
				645					650					655		
ggg Gly	ttg Leu	aca Thr	aat Asn	atc Ile	aag Lys	acg Thr	gag Glu	gag Glu	atc Ile	tct Ser	gaa Glu	gtg Val	aag Lys	atg Met	gat Asp	2016
			660					665					670			
gca Ala	gaa Glu	ttc Phe	cga Arg	cat His	gac Asp	tca Ser	gga Gly	tat Tyr	gaa Glu	gtt Val	cat His	cat His	caa Gln	aaa Lys	ttg Leu	2064
		675					680					685				

gtg ttc ttt gca gaa gat gtg ggt tca aac aaa ggt gca atc att gga 2112
Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly
690 695 700

ctc atg gtg ggc ggt gtt gtc ata gcg aca gtg atc gtc atc acc ttg 2160
Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu
705 710 715 720

gtg atg ctg aag aag aaa cag tac aca tcc att cat cat ggt gtg gtg 2208
Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val
725 730 735

gag gtt gac gcc gct gtc acc cca gag gag cgc cac ctg tcc aag atg 2256
Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met
740 745 750

cag cag aac ggc tac gaa aat cca acc tac aag ttc ttt gag cag atg 2304
Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met
755 760 765

cag aac tag 2313
Gln Asn
770

<210> 2
<211> 770
<212> PRT
<213> Homo sapiens

<400> 2

Met Leu Pro Gly Leu Ala Leu Leu Leu Leu Ala Ala Trp Thr Ala Arg
1 5 10 15

Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
20 25 30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
35 40 45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
50 55 60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
85 90 95

09758250

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
210 215 220

Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu
225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
260 265 270

Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
275 280 285

Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile
290 295 300

Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe
305 310 315 320

Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp
545 550 555 560

Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val
565 570 575

Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala
580 585 590

Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr Val Glu Leu Leu Pro
595 600 605

Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe
610 615 620

Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val
625 630 635 640

Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser
645 650 655

Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp
660 665 670

Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu
675 680 685

Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly
690 695 700

Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu
705 710 715 720

Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val
725 730 735

Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met
740 745 750

Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met
755 760 765

Gln Asn
770

<210> 3
<211> 45
<212> DNA
<213> Clostridium tetani

<220>
<221> CDS
<222> (1)..(45)
<223> DNA encoding P2 epitope

<400> 3
cag tac atc aaa gct aac tcc aaa ttc atc ggt atc acc gag ctg 45
Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu
1 5 10 15

<210> 4
<211> 15
<212> PRT
<213> Clostridium tetani

<400> 4
Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu
1 5 10 15

<210> 5
<211> 63
<212> DNA
<213> Clostridium tetani

<220>
<221> CDS
<222> (1)..(63)
<223> DNA encoding P30 epitope

<400> 5
ttc aac aac ttc acc gta agc ttc tgg ctg cgt gtt ccg aaa gtt agc 48
Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser
1 5 10 15

gct agc cac ctg gaa 63
Ala Ser His Leu Glu
20

<210> 6
<211> 21

<212> PRT
<213> Clostridium tetani

<400> 6

Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser
1 5 10 15

Ala Ser His Leu Glu
20

<210> 7
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer targeted to the pAB1 plasmid

<400> 7
caactcagct tcctttcggg c 21

<210> 8
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer targeted to the pAB1 plasmid

<400> 8
agatctcgat cccgcgaaat t 21

<210> 9
<211> 135
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer that encodes the human abeta-43 fragment with E. coli
optimised codons

<400> 9
atggatgcag aattccgtca cgactccggt tacgaagttc accaccagaa actgggttttc 60
ttcgcagaag atgttggttc caacaaaggt gcaatcatcg gtctgatggt tggcgggtgtt 120
gttatcgcga cctag 135

<210> 10
<211> 31

<212> DNA
<213> Artificial Sequence

<220>
<223> Primer derived from SEQ ID NO:9

<400> 10
gccggccatg gatgcagaat tccgtcacga c 31

<210> 11
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer derived from SEQ ID NO:9

<400> 11
gccggaagct tctaggctgc gataacaaca ccgccaacc 39

<210> 12
<211> 84
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer encoding the P2 epitope

<400> 12
ccggcaagct tctacagctc ggtgataccg atgaatttgg agttagcttt gatgtactgg 60
gtcgcgataa caacaccgcc aacc 84

<210> 13
<211> 101
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer derived from the pAB1 plasmid

<400> 13
gccggccatg gggttcaaca acttcaccgt tagcttctgg ctgcgtgttc cgaaagttag 60
cgcgagccac ctggaagatg cagaattccg tcacgactcc g 101

<210> 14
<211> 172
<212> DNA
<213> Artificial Sequence

<220>

<223> Primer derived from the pAB2 plasmid

<400> 14

gggccaagct tggatccggt cgcgataaca acaccgcca ccatcagacc gatgattgca 60

cctttgttgg aaccaacatc ttctgcgaag aaaaccagtt tctggtggtg aacttcgtaa 120

ccggagtcgt gacggaactc tgcattccagc tcggtgatac cgatgaattt gg 172

<210> 15

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer derived from the pAB3 plasmid

<400> 15

ctggaagatg cagagttccg tcacgactcc 30

<210> 16

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer derived from the pAB3 plasmid

<400> 16

gcgcgcatc cttcaacaac ttcaccgtta gcttc 35

<210> 17

<211> 8

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificial sequence, used as an example for how to calculate sequence identity, has 75% sequence identity with SEQ ID NO:18

<400> 17

agtcagtc 8

<210> 18

<211> 8

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificial sequence, used as an example for how to calculate sequence identity, has 75% sequence identity with SEQ ID NO:17

<400> 18
aatcaatc

8

<210> 19
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> artificial T-cell epitope capable of binding to a large portion
of MHC Class II molecules in a variety of animals

<400> 19

Ala Lys Phe Val Ala Ala Trp Thr Leu Lys Ala Ala Ala
1 5 10

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